

SEQUENCE LISTING

<110> Hope, Ernest G.
Negrin, Robert

<120> COMPOSITIONS AND METHODS FOR PROTECTING
ORGANS, TISSUE AND CELLS FROM IMMUNE SYSTEM-MEDIATED DAMAGE

<130> 12932-003001

<140> US 09/382,088

<141> 1999-08-24

<150> US 60/097,640

<151> 1998-08-24

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 2

<223> Xaa = Val, Leu, Ala, or Thr

<221> VARIANT

<222> 3

<223> Xaa = Leu or His

<221> VARIANT

<222> 4

<223> Xaa = Ser or Val

<221> VARIANT

<222> 6

<223> Xaa = Asp or Glu

<221> VARIANT

<222> 7

<223> Xaa = Gln, Lys, or Arg

<221> VARIANT

<222> (8)...(8)

<223> Xaa = Leu or Val

<400> 1

Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg

1

5

B

<210> 2
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
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 <223> Xaa = Val or Ala

<221> VARIANT
 <222> 3
 <223> Xaa = Leu or His

<221> VARIANT
 <222> 4
 <223> Xaa = Ser or Val

<400> 2
 Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg
 1 5

<210> 3
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 3
 Ala Val Leu Ser Ala Glu Gln Leu Arg
 1 5

<210> 4
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 4
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 ggagccgctt tgggtgtccc gcaccaggaa gatgaagggg tggtcggcgt agaacagctt 120
 ggggctgctc agctcctcgc gcccgtagat gtcttggtca aaggggttgc catctgtgtc 180
 caactcaaag gcggtggcgt ggaacacact ggccaggtag agatccttct tgccagacat 240
 gcgtagataag tccgccttgt tcttgtcaat ggctcagtc aggccagacc cagccagggtg 300
 tttctgcagg tcatgggtca cctccaccac acccttgggc aaggagatgg caacagcctt 360
 cttctgcata tccccatcc agatcttcag ctgctctttg gttagcagct tttcaaggcg 420
 ctcgagaggg tccacgtgat ggggcatgag gatgatgagg ctggagagct tgtgagccag 480
 gggcatctcc accagctgca gcttctcctt ctgctcgtcg tagtagttgt agaggcctgt 540
 ccggtgcatc atcgtaacac ccacagtata ggaccgagtc accatgaagc cacggttgctc 600
 caccatcttg tgggtggaatt tctcatccca gtgtggcctt aagaacatgg cgttgactag 660
 cagggcgccg tccgtgctct ccacgtcctt ggtgacctcg ggcagcttgc cgtcggtggt 720
 ctgcgcggcc cactcggtga tggactgcag cgcgctgcgc ttgtccggga agttgatctt 780
 ggagtgtctg cagttgtagt gctgcttgct gctcgccacg aagtcacag cgaagctcac 840
 tgagctgggt ccgtacagtc ggctgcccag cttccaggtc acgttgccgc ccgtcgagtt 900
 gctgagtgag cgcagcagct caccagggc ggcgtgcacc tctcgtcgc gcagctgctc 960
 ggcgctcagc actgccttgg cctgcgacgc cgtggtcgcc ttgccgccca gcgacacgag 1020

```

accagcgac gaggccacca ccacgggtga caccaggatg ttctccactg cctgggtcctt 1080
ggccattgcc tgatacaggc tgaaggccag gcctgtgctg ggctctgccca gtgtgggtcgc 1140
cttggaactc agcttctccg cagtaccagg ggctgcggcc tctacaggtt tcttcacctc 1200
ggctgccagg gccacagcca ggaggcataa ggtgcccaga aggagagagc gcat 1254

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<210> 5

<211> 1254

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1251)

<400> 5

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atg cgc tct ctc ctt ctg ggc acc tta tgc ctc ctg gct gtg gcc ctg 48
Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
1 5 10 15

```

```

gca gcc gag gtg aag aaa cct gta gag gcc gca gcc cct ggt act gcg 96
Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
20 25 30

```

```

gag aag ctg agt tcc aag gcg acc aca ctg gca gag ccc agc aca ggc 144
Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
35 40 45

```

```

ctg gcc ttc agc ctg tat cag gca atg gcc aag gac cag gca gtg gag 192
Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
50 55 60

```

```

aac atc ctg gtg tca ccc gtg gtg gtg gcc tcg tcg ctg ggt ctc gtg 240
Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
65 70 75 80

```

```

tcg ctg ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg 288
Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
85 90 95

```

```

agc gcc gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggt gag 336
Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
100 105 110

```

```

ctg ctg cgc tca ctc agc aac tcg acg gcg cgc aac gtg acc tgg aag 384
Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
115 120 125

```

```

ctg ggc agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac 432
Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
130 135 140

```

```

ttc gtg gcg agc agc aag cag cac tac aac tgc gag cac tcc aag atc 480
Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
145 150 155 160

```

```

aac ttc ccg gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc 528
Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala

```

165	170	175	
gcg cag acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu 180 185 190			576
agc acg gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His 195 200 205			624
tgg gat gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met 210 215 220			672
gtg act cgg tcc tat act gtg ggt gtt acg atg atg cac cgg aca ggc Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly 225 230 235 240			720
ctc tac aac tac tac gac gac gag aag gag aag ctg cag ctg gtg gag Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu 245 250 255			768
atg ccc ctg gct cac aag ctc tcc agc ctc atc atc ctc atg ccc cat Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His 260 265 270			816
cac gtg gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln 275 280 285			864
ctg aag atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser 290 295 300			912
ttg ccc aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu 305 310 315 320			960
gct ggg ctg ggc ctg act gag gcc att gac aag aac aag gcc gac tta Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu 325 330 335			1008
tca cgc atg tct ggc aag aag gat ctg tac ctg gcc agt gtg ttc cac Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His 340 345 350			1056
gcc acc gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp 355 360 365			1104
atc tac ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp 370 375 380			1152
cac ccc ttc atc ttc ctg gtg cgg gac acc caa agc ggc tcc ctg cta His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu 385 390 395 400			1200

ttc att ggg cgc ctg gtc cgg ctc aag ggt gac aag atg cga gac gag
 Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
 405 410 415

1248

tta tag
 Leu

1254

<210> 6
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 6
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 Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
 20 25 30
 Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
 35 40 45
 Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
 50 55 60
 Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
 65 70 75 80
 Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
 85 90 95
 Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
 100 105 110
 Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
 115 120 125
 Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
 130 135 140
 Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
 145 150 155 160
 Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
 165 170 175
 Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
 180 185 190
 Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
 195 200 205
 Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
 210 215 220
 Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
 225 230 235 240
 Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
 245 250 255
 Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
 260 265 270
 His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
 275 280 285
 Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
 290 295 300
 Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
 305 310 315 320
 Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu

				325					330					335					
Ser	Arg	Met	Ser	Gly	Lys	Lys	Asp	Leu	Tyr	Leu	Ala	Ser	Val	Phe	His				
			340					345					350						
Ala	Thr	Ala	Phe	Glu	Leu	Asp	Thr	Asp	Gly	Asn	Pro	Phe	Asp	Gln	Asp				
		355					360					365							
Ile	Tyr	Gly	Arg	Glu	Glu	Leu	Arg	Ser	Pro	Lys	Leu	Phe	Tyr	Ala	Asp				
	370					375					380								
His	Pro	Phe	Ile	Phe	Leu	Val	Arg	Asp	Thr	Gln	Ser	Gly	Ser	Leu	Leu				
385					390					395					400				
Phe	Ile	Gly	Arg	Leu	Val	Arg	Leu	Lys	Gly	Asp	Lys	Met	Arg	Asp	Glu				
				405					410					415					

Leu

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 7

Ala Ala His Val Ala Glu Gln Leu Arg

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<210> 8

<211> 9

<212> PRT

<213> Rattus norvegicus

<400> 8

Ala Val Leu Ser Ala Glu Lys Leu Arg

1

5

<210> 9

<211> 9

<212> PRT

<213> Gallus gallus

<400> 9

Ala Val Leu Ser Ala Asp Lys Leu Asn

1

5

<210> 10

<211> 9

<212> PRT

<213> Homo sapiens

<400> 10

Ala Thr Leu Ser Ala Glu Arg Val Arg

1

5

<210> 11

<211> 9

<212> PRT

<213> Felis catus

<400> 11
Ala Thr Leu Ser Ala Glu Lys Val Arg
1 5

<210> 12
<211> 9
<212> PRT
<213> Bos taurus

<400> 12
Ala Leu Leu Ser Ala Glu Lys Val Asn
1 5

<210> 13
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 6
<223> Xaa = Asp or Glu

<221> VARIANT
<222> 7
<223> Xaa = Lys or Gln

<400> 13
Ala Val Leu Ser Ala Xaa Xaa Leu Arg
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<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Val, Leu, or Thr

<221> VARIANT
<222> 7
<223> Xaa = Gln, Lys, or Arg

<221> VARIANT
<222> 8
<223> Xaa = Leu or Val

<400> 14
Ala Xaa Leu Ser Ala Glu Xaa Xaa Arg
1 5

<210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 15
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<210> 16
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 16
 gtccttggcc at 12

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 17
 gcaatggcca aggaccaggc agtggag 27

<210> 18
 <211> 27
 <212> DNA
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<220>
 <223> primer for PCR

<400> 18
 atctgaattc ctataactcg tctcgca 27

<210> 19
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 19
 Lys Asp Glu Leu
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<210> 20
 <211> 4
 <212> PRT

<213> Homo sapiens

<400> 20

Arg Asp Glu Leu

1

<210> 21

<211> 17

<212> PRT

<213> Homo sapiens

<400> 21

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Ala

<210> 22

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<213> Homo sapiens

<400> 22

Arg Val Glu Leu

1

<210> 23

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 23

cggaattctg gccgaggtga agaaacc

27

<210> 24

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 24

agttcccact gttctacgac ctagggc

27

<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 25

aactcaacct gtgtctagac ctatgggc

28

<210> 26
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 26
 acgcgctgct cctccacgac ctagggc

27

<210> 27
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 <212> PRT
 <213> Artificial Sequence

<220>
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 <222> 2, 4
 <223> Xaa = Val or Ala

<221> VARIANT
 <222> 3
 <223> Xaa = Leu or His

<400> 27
 Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg
 1 5

<210> 28
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> VARIANT
 <222> 2
 <223> Xaa = Val, Leu, Ala, or Thr

<221> VARIANT
 <222> 3
 <223> Xaa = Leu or His

<221> VARIANT
 <222> 4
 <223> Xaa = Ala or Val

<221> VARIANT
 <222> 6
 <223> Xaa = Asp or Glu

<221> VARIANT
<222> 7
<223> Xaa = Lys, Gln, or Arg

<221> VARIANT
<222> (8)...(8)
<223> Xaa = Leu or Val

<400> 28
Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg
1 5

<210> 29
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> (1)...(9)
<223> Xaa = any amino acid

<400> 29
Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg
1 5
